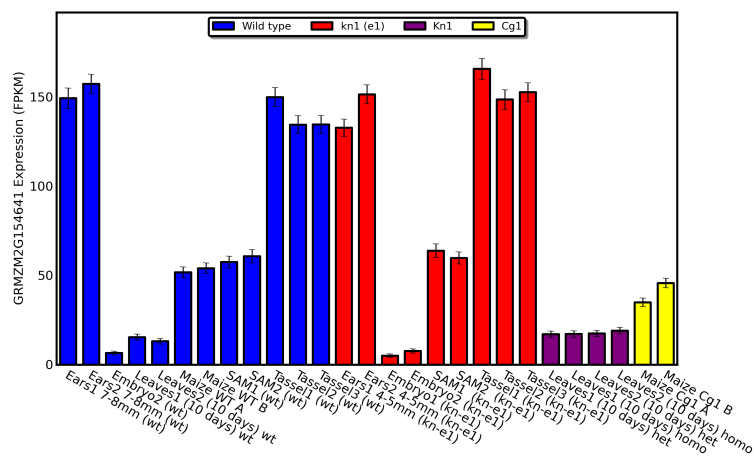
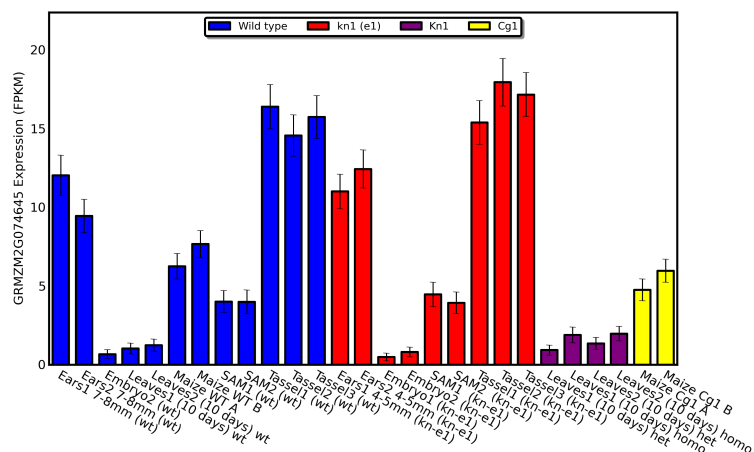


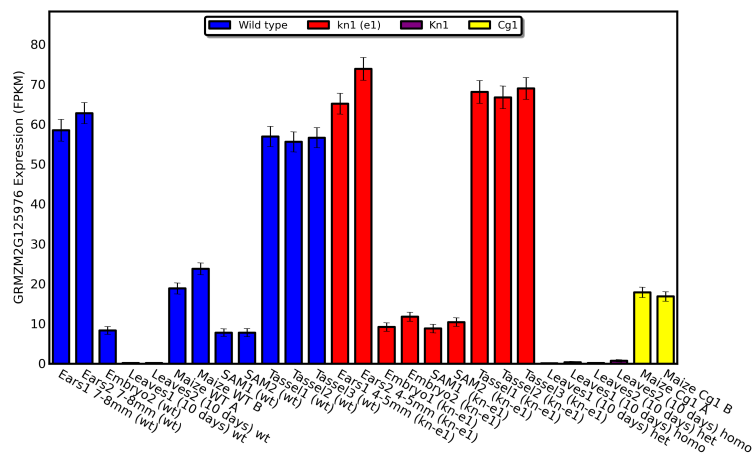
A

*blh12*

B

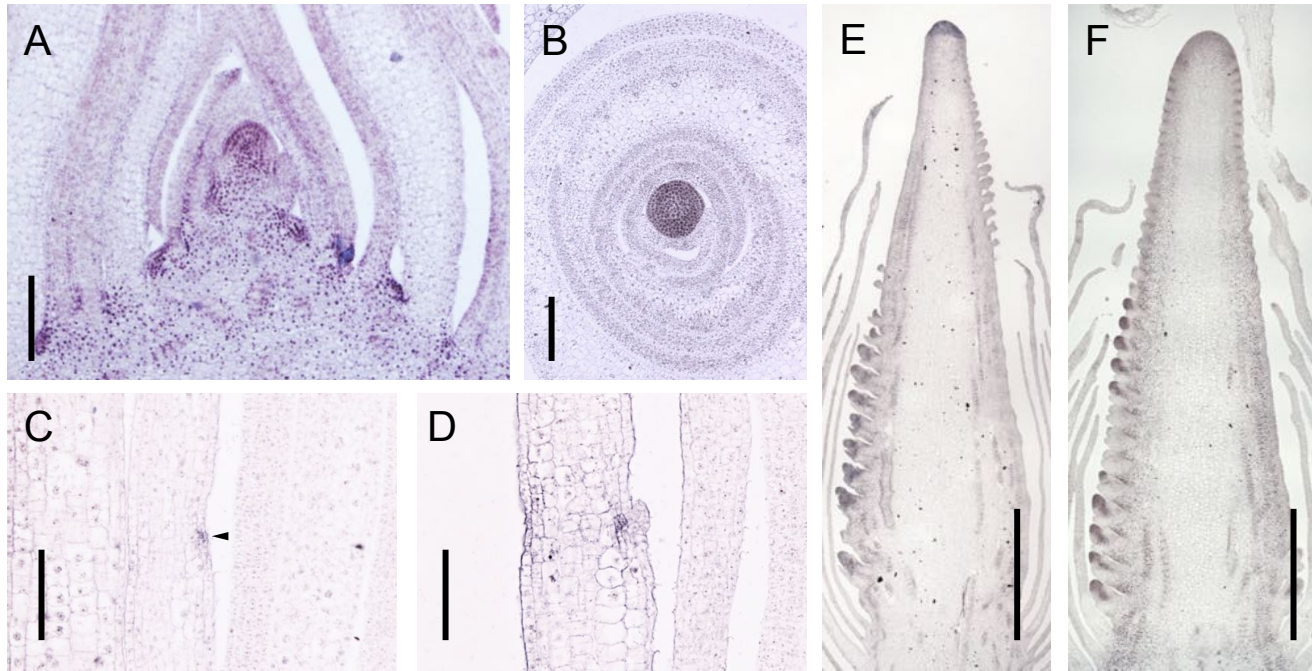
*blh13*

C

*blh14*

### Supplemental Figure 1. Relative expression levels of *BLH* genes in various tissues, supporting Figure 1.

Relative expression levels of *blh12*, *blh13* and *blh14* are shown in (A), (B) and (C), respectively. Data were obtained from qTeller (<http://www.qteller.com/>). Data represent mean values of three biological replicates and error bars are SD. *kn1-e1* is a loss-of-function allele of *kn1*.



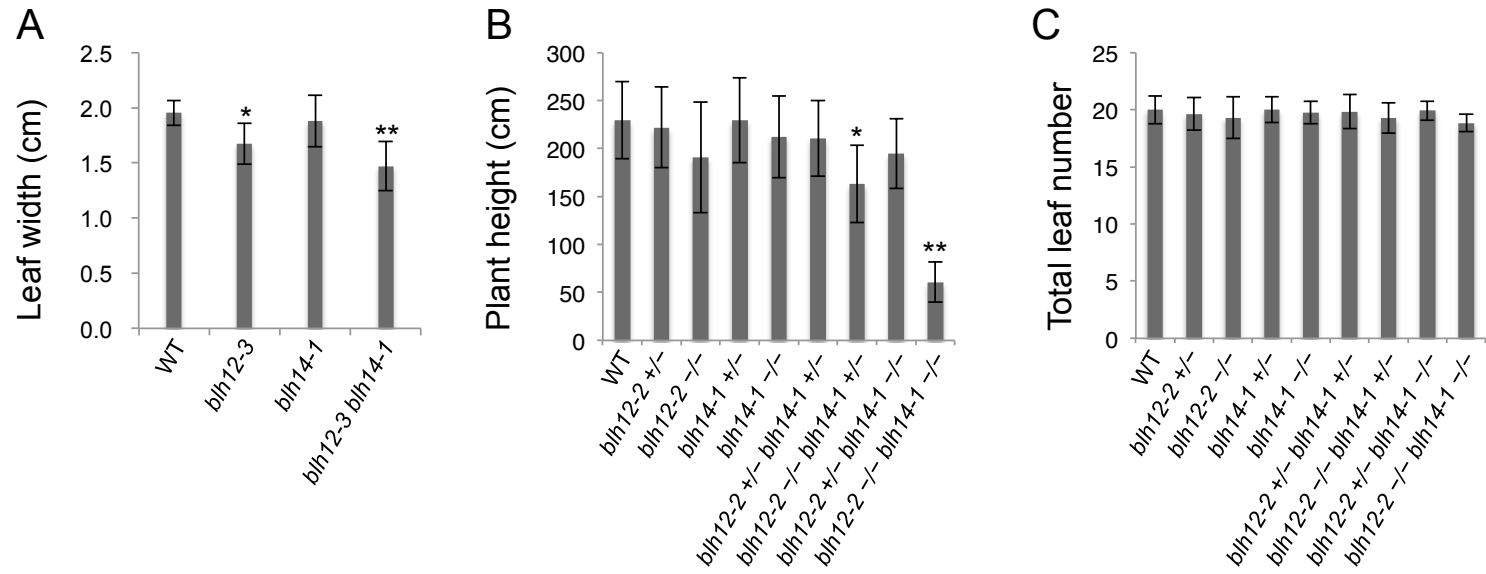
**Supplemental Figure 2. Accumulation patterns of BLH12 and BLH14 in wild type, supporting Figure 2.**

**(A and B)** Immunostaining reveals BLH12 expression in entire SAM. (A) and (B) are vertical and horizontal sections, respectively.

**(C and D)** Immunostaining of BLH14 in the preligule regions (an arrowhead) in (C) and in the developing ligule in (D).

**(E and F)** Immunostaining of BLH12 in (E) and of BLH14 in (F) in the young ear.

Bars represent 200  $\mu$ m in (A) and (B), 100  $\mu$ m in (C) and (D), and 1 mm in (E) and (F), respectively.



**Supplemental Figure 3. Measurement of plant height and leaf number in *blh12/14* mutants, supporting Figure 3.**

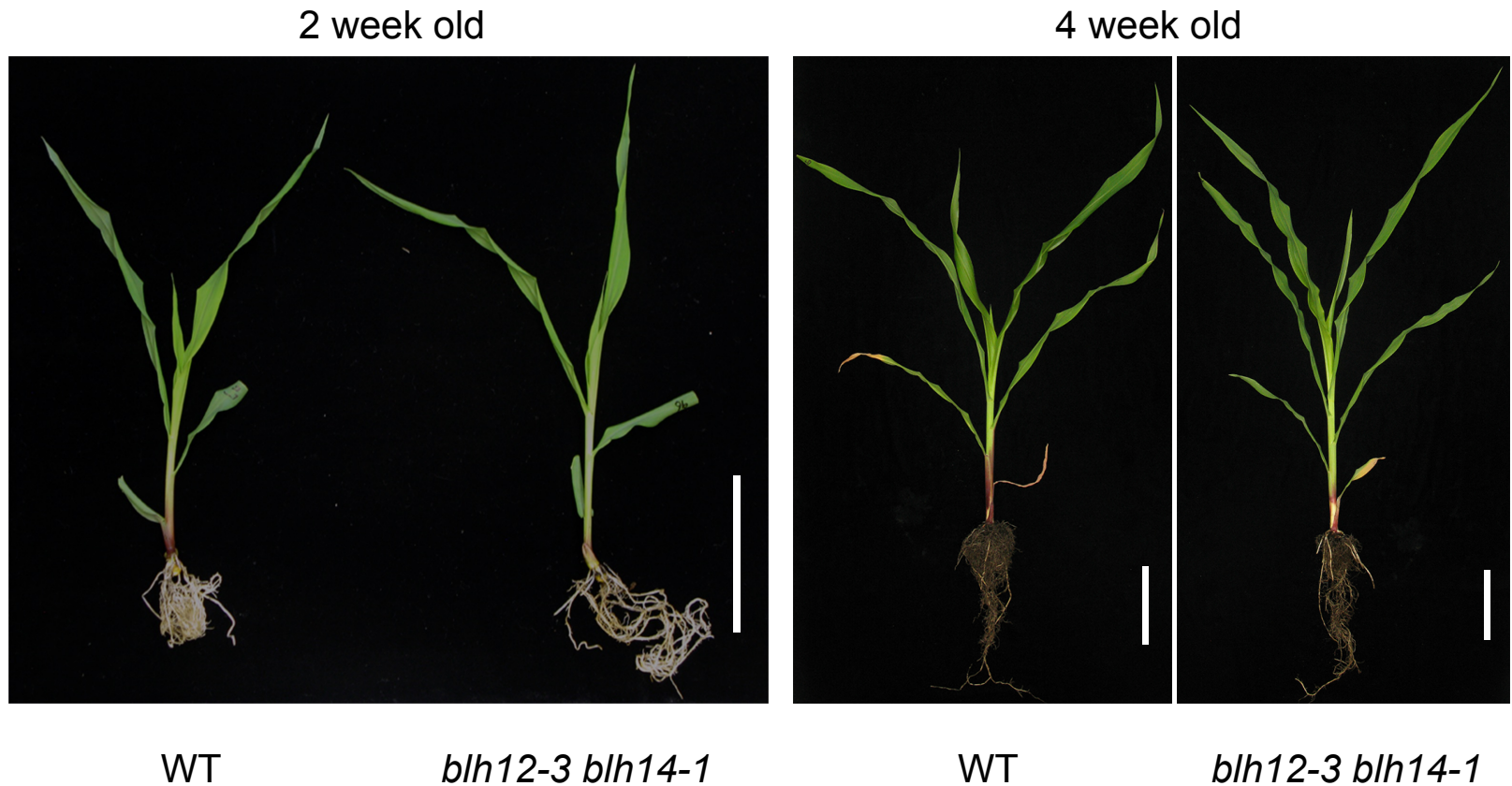
**(A)** Leaf width at 3 weeks old. The width was measured at the middle of fourth leaf blades ( $n = 10$ ).  $p$ -values for single and double asterisks are  $1.51\text{E-}04$  and  $8.01\text{E-}05$ , respectively.

**(B)** Plant height at maturity.  $p$ -values for single and double asterisks are  $1.60\text{E-}06$  and  $1.06\text{E-}17$ , respectively.

**(C)** Total leaf number at maturity.

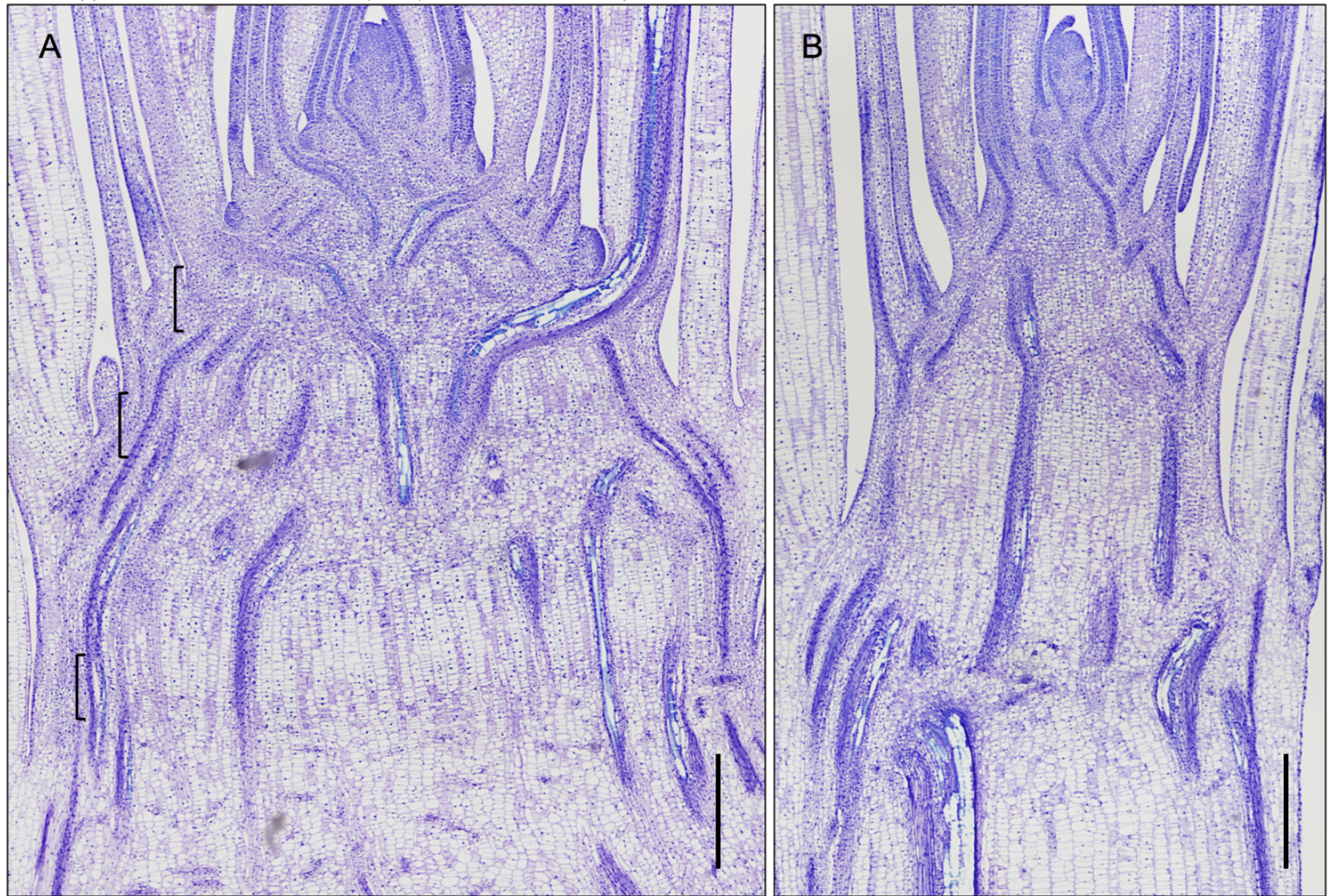
Measurements were performed using at least 11 plants in each genotype.

Error bars represent SD. WT, wild type.



**Supplemental Figure 4. Double mutant phenotypes during vegetative growth, supporting Figure 4.**  
Wild type (WT, left) and *blh12-3 blh14-1* (right) double mutant seedlings at 2 and 4 weeks old. Scale bars are 5 cm.

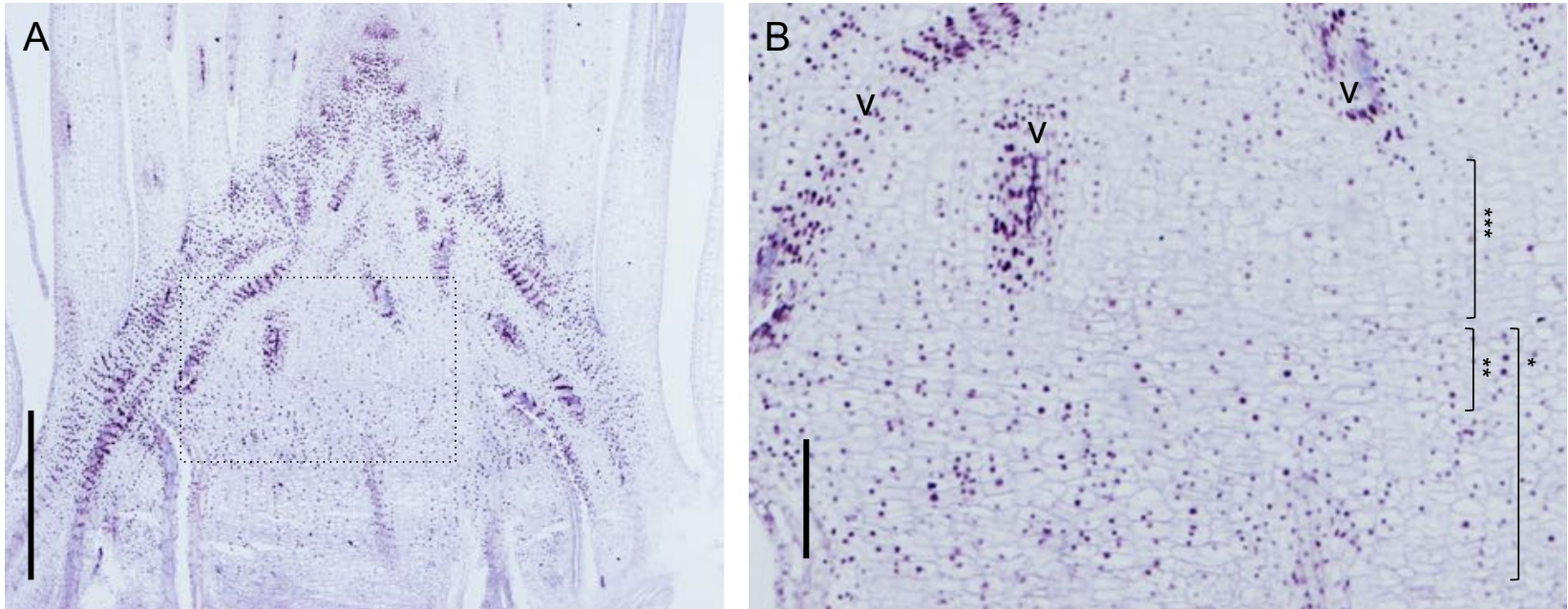




**Supplemental Figure 5. Tissue sections of stems at 4 weeks old, supporting Figure 4.**

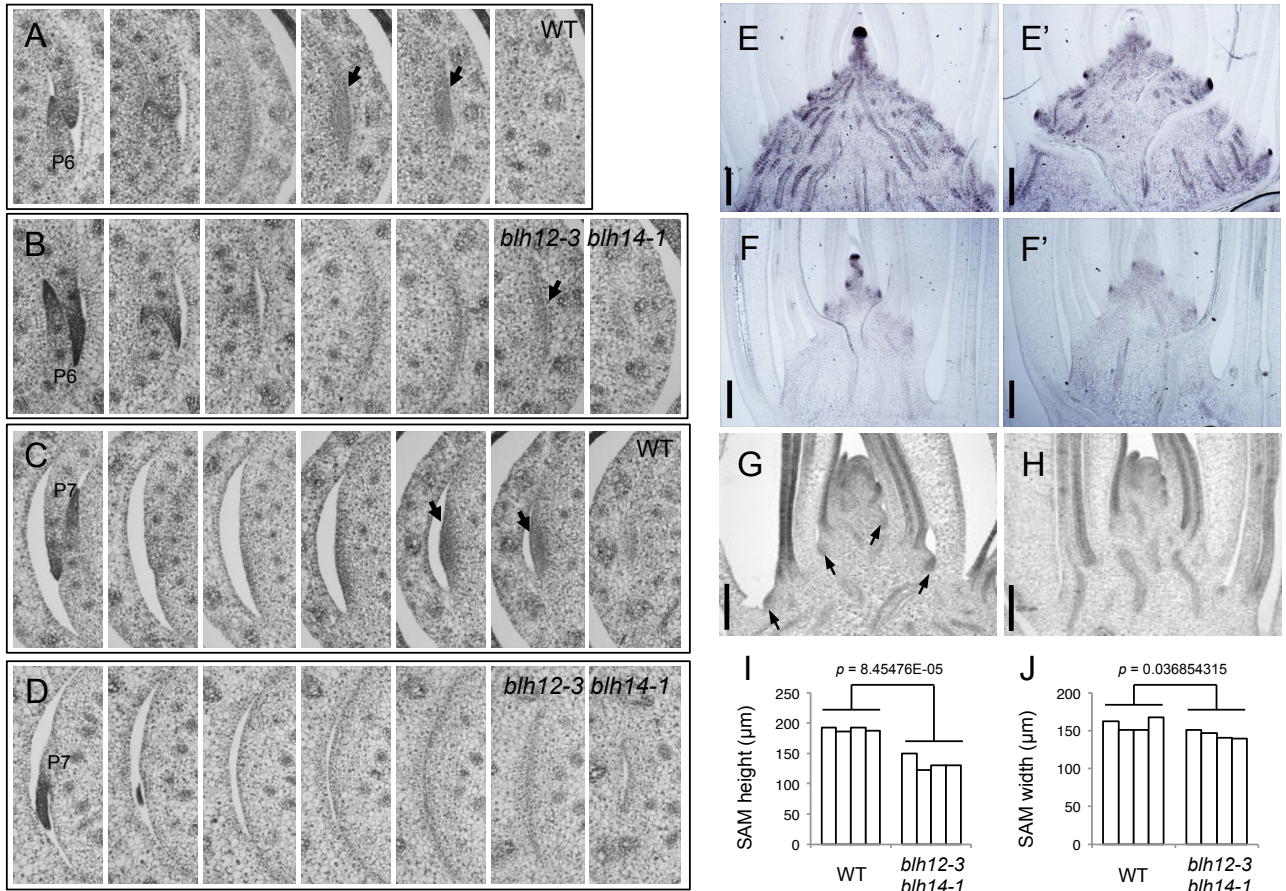
(A) A higher resolution image of Figure 4A (wild type). Intercalary meristems (bands of actively dividing cells) are marked with brackets. (B) A higher resolution image of Figure 4C (*blh12-3 blh14-1*) double mutants. Scale bars are 400 μm.





**Supplemental Figure 6. Immunostaining of BLH12 in the young stem, supporting Figure 4.**

The box in (A) represents the magnified region in (B). Bars are 500  $\mu\text{m}$  in (A) and 100  $\mu\text{m}$  in (B). Brackets with single, double and triple asterisks indicate a nodal region, a putative intercalary meristem and an internode, respectively. v: accumulation of BLH12 in provascular bundles.



**Supplemental Figure 7. Phenotypes of *blh12-3 blh14-1* vegetative shoot apices, supporting Figure 5.**

(A-D) Serial sections of P6 (A and B) and P7 (C and D) leaf axils in wild type (WT, A and C) and in *blh12-3 blh14-1* (B and D) at 4 weeks old.

(E and F) KN1 immunostaining in wild type (E) and *blh12-3 blh14-1* (F) at 4 weeks old. (E') and (F') are additional sections from same plants in (E) and (F), respectively, to show the KN1 expression in the axillary meristems. Scale bars are 400 μm.

(G) Tissue section of wild-type SAM.

(H) Tissue section of *blh12-3 blh14-1* SAM.

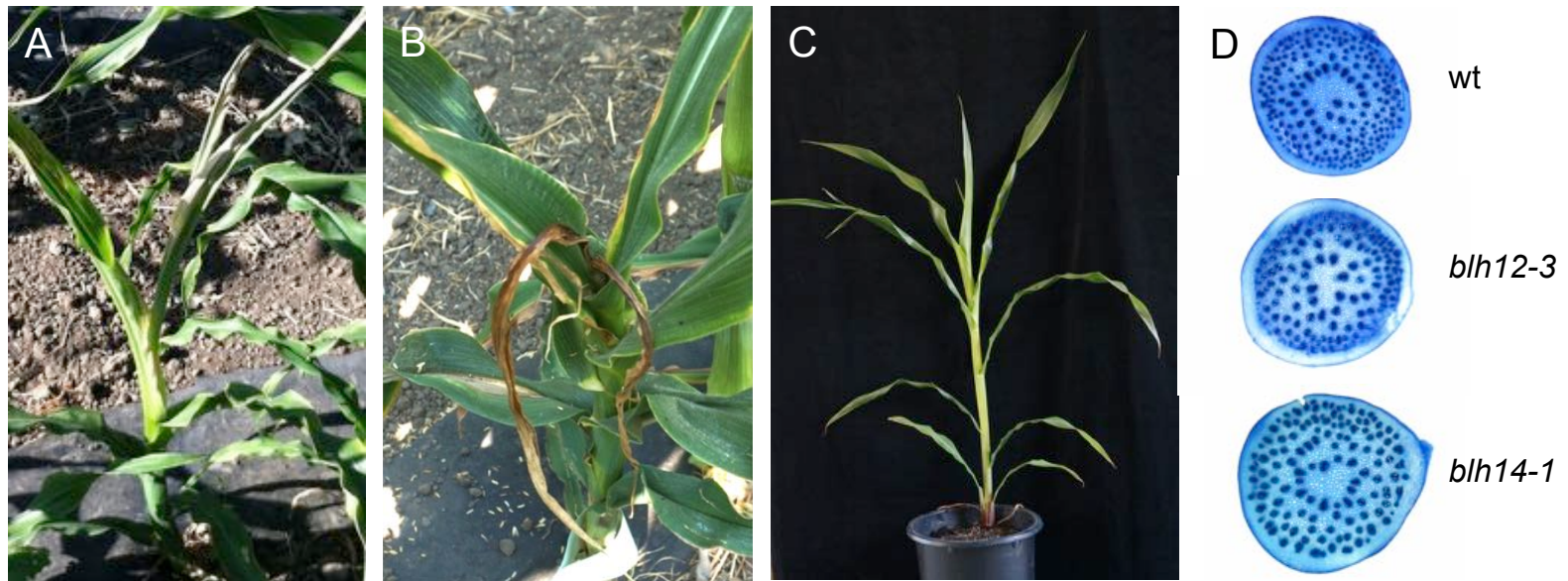
(I) Measurement of SAM height (n=4).

(J) Measurement of SAM width (n=4).

*p*-values in Student's *t*-test are indicated in (I) and (J). E represents exponent in the *p*-value.

Arrows indicate nucleocytoplasmic cells in axillary meristems.





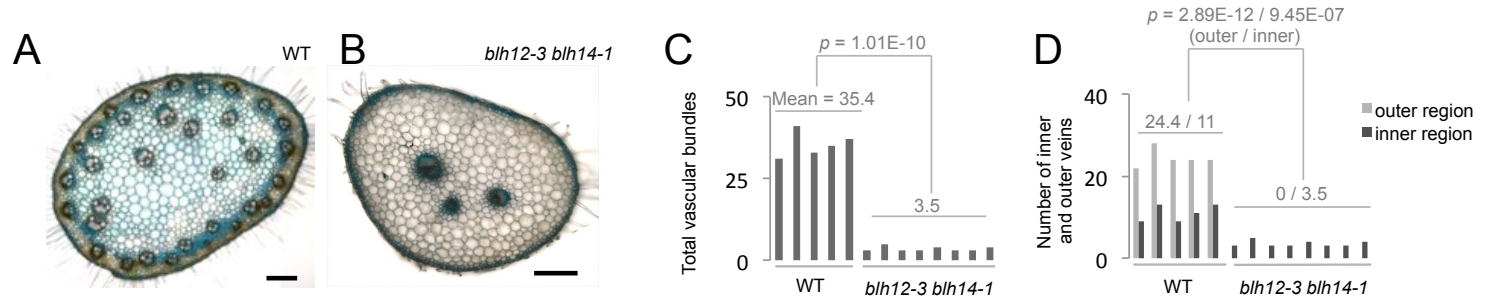
**Supplemental Figure 8. Leaf drought phenotype of *blh12-3 blh14-1* grown in summer field conditions, supporting Figure 6.**

(A) Drought phenotype at 7 weeks old. A few leaves from the top are curled and became chlorotic.

(B) Drought phenotype at maturity. A few leaves from the top died.

(C) A *blh12-3 blh14-1* at 7 weeks old grown in the greenhouse. Top leaves are green and not curled.

(D) Both *blh12-3* and *blh14-1* single mutants had comparable numbers of veins to wild type in the stem.



**Supplemental Figure 9. Fewer vascular bundles form in *blh12-3 blh14-1* tassel branches, supporting Figure 6.**

**(A and B)** Transverse hand sections of wild-type (A) and *blh12-3 blh14-1* (B) tassel branches.

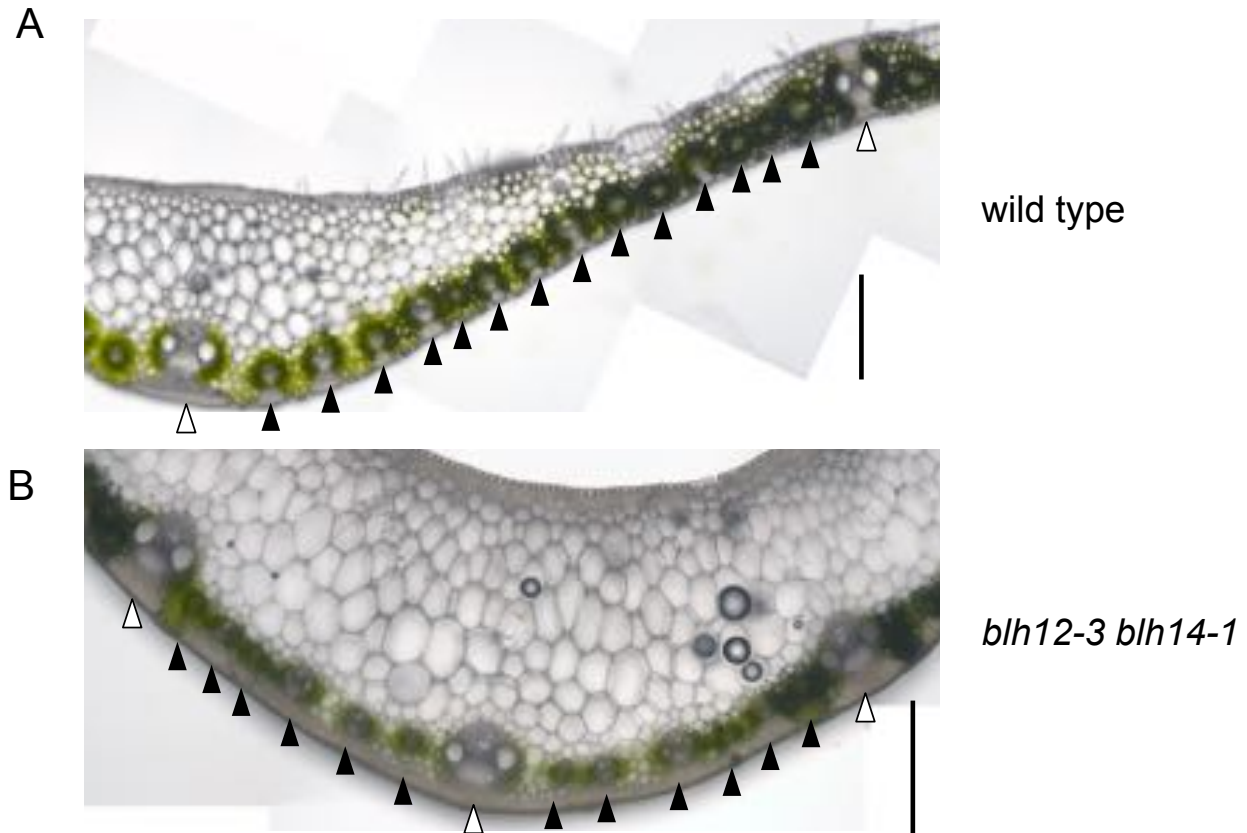
Bars are 200  $\mu\text{m}$ .

**(C)** Total number of vascular bundles in the tassel branches.

**(D)** Measurement of vascular bundles in inner and outer regions of tassel rachises.

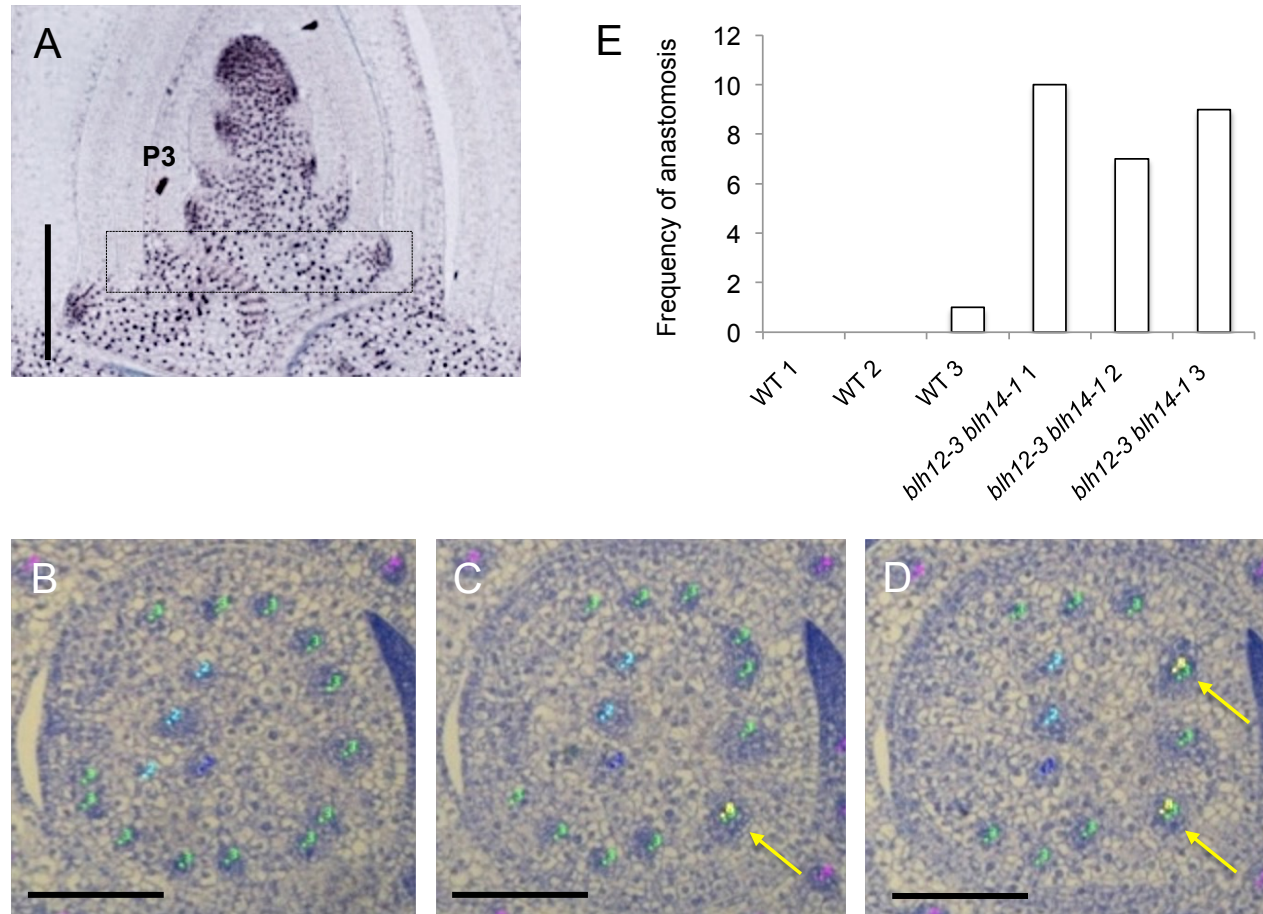
Vein numbers were counted in five and eight tassel branches in wild type and *blh12-3 blh14-1*, respectively. Mean values and  $p$ -values in Student's  $t$ -test are represented in (C) and (D). E in  $p$ -value represents exponent. WT, wild type.





**Supplemental Figure 10. Transverse sections of leaf blades formed below tassels, supporting Figure 6.**

Hand sections of wild type (A) and *blh12-3 blh14-1* (B) mature leaf blades. White and black arrowheads represent lateral and intermediate veins, respectively. Scale bars are 500  $\mu$ m.



**Supplemental Figure 11. Veins precociously fuse just below the SAM in *blh12-3 blh14-1*, supporting Figure 7.**

**(A)** The region marked with a box represents the level of cross sections shown in (B to D). A scale bar is 200  $\mu$ m.

**(B to D)** Serial sections from top (B) to bottom (D) of *blh12-3 blh14-1* young stem. Provascular bundles from P3 leaf primordium are marked with green. Yellow arrows represent anastomosed veins. Provascular bundles are marked with numbers according to leaf primordia numbers in same color (e.g. P1 is 1 in blue). Scale bars are 200  $\mu$ m.

**(E)** Frequency of anastomosis observed in SAM-P5 young stem regions counted in Supplemental Movie 4 and 5. Data from three individuals are represented for each genotype.

<b>genotype</b>	wild type	<i>blh12-2</i> +/-	<i>blh12-2</i> -/-	<i>blh14-1</i> +/-	<i>blh14-1</i> -/-	<i>blh12-2</i> +/- <i>blh14-1</i> +/-	<i>blh12-2</i> -/- <i>blh14-1</i> +/-	<i>blh12-2</i> +/- <i>blh14-1</i> -/-	<i>blh12-2</i> -/- <i>blh14-1</i> -/-
plant with tiller / total (%)	7/22 (32)	20/42 (48)	7/11 (64)	18/46 (39)	9/27 (33)	33/70 (47)	11/23 (48)	10/23 (43)	0/15 (0)

**Supplemental Table 1. Numbers of individuals that produced tillers in the family segregating *blh12-2 blh14-1* double mutants, supporting Figure 5.**

Supplemental Table 2. Oligo DNA sequences

Experiment	Forward primer	Sequence	Reverse primer	Sequence
<i>blh12-1</i> genotyping wt allele	KT306	tcacctgtcccgggtctctct	KT307	gacgcgtaggagtagaacgc
<i>blh12-1</i> genotyping Mu inserted allele	KT306	see above	TIR6	agagaagccaacgccawcgctcyatttcgtc
<i>blh12-2</i> genotyping wt allele	KT644	ttcgacatatcatattgctcaaccgtgg	KT549	gttacctgccctgctgaatag
<i>blh12-2</i> genotyping Mu inserted allele	KT549	see above	TIR6	see above
<i>blh12-3</i> genotyping wt allele	KT645	cagagttctttaatggcatcccg	KT646	agagccaagcgcggaacag
<i>blh12-3</i> genotyping Mu inserted allele	KT646	see above	TIR6	see above
<i>blh14-1</i> genotyping wt allele	KT547	gtatgctcgacatggacg	KT548	cagcaagaacttcacagcaagttgc
<i>blh14-1</i> genotyping Mu inserted allele	KT548	see above	TIR6	see above
BLH12 CDS cloning into pENTR	KT543	caccATGTCGTCCGCCGCGGGCGGGTATG	KT544	TCAGCCAACAAAATCATGCACCAAATG
BLH14 CDS cloning into pENTR	KT545	caccATGTCCTCGGCGGCGGGCGGTGGATAC	KT546	TCAACCGACAAAGTCATGGAGCAAG
NLS-RFP construction	GW SV40WT F	CACCatgTGCACTCCGCCGAAGAAGAAGCGTAAGGTG	GW SV40WT R	CACCTTACGCTTCTTCTTCGGCGGAGTGCAcatGGTG

Supplemental Table 3. Gene IDs and Accession Numbers.

Gene Name	ID	Accession Number
ATH1	AT4G32980.1	AY096513.1
BEL1	AT5G41410.1	AY049237
BLH1/EDA29	AT2G35940.1	AY096548
BLH2/SAW1	AT4G36870.1	AY050459
BLH3	AT1G75410.1	BT000133
BLH4/SAW2	AT2G23760.1	AY142019
BLH5	AT2G27220.2	AB493565
BLH6	AT4G34610.1	BT012291
BLH7	AT2G16400.1	AY056796
BLH8/PNF	AT2G27990.1	BT005921
BLH9/PNY	AT5G02030.1	AY084243
BLH10	AT1G19700.1	AY570508
BLH11	AT1G75430.1	AB493535
ZmBLH1	GRMZM2G161435	AFW71261.1
ZmBLH2	GRMZM2G333565	AFW73753.1
ZmBLH3	GRMZM2G142700	DAA35928.1
ZmBLH4	GRMZM2G458728	AFW65585.1
ZmBLH5	GRMZM2G099319	DAA47673.1
ZmBLH6	GRMZM2G148098	AFW67987.1
ZmBLH7	GRMZM2G004641	DAA43547.1
ZmBLH8	GRMZM2G396114	DAA51178.1
ZmBLH9	GRMZM2G327059	DAA43037.1
ZmBLH10	GRMZM2G013617	AFW75230.1
ZmBLH11	GRMZM2G064466	DAA46067.1
ZmBLH12	GRMZM2G154641	DAA56836.1
ZmBLH13	GRMZM2G074645	AFW81703.1
ZmBLH14	GRMZM2G125976	AFW78222.1
ZmBLH15	GRMZM2G011588	DAA50500.1
ZmBLH16/KIP	GRMZM2G163761	DAA50503.1
ZmBLH17	GRMZM2G076272	AFW86670.1
ZmBLH18	GRMZM2G458755	GRMZM2G458755_T02